

1 **Supplementary material to:**

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3 **Complete genome sequence of the heavy metal resistant bacterium**
4 ***Agromyces aureus* AR33^T and comparison with related Actinobacteria**

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13 **Table S1**

14 **Table S1.** Primers used to close the gaps between the four contigs from the preliminary assembly.
15 First, primers were designed at the edges (start/end) of each contig. In this way, we could determine
16 that contig C4 (containing the rRNA genes) was positioned at the start and end of the other three
17 contigs. Then, the three gaps (circa 6 kb) were cloned and sequenced with the specific primers listed in
18 this table.

Primers	Sequence 5'-3'
C1-start	GGTGTGCGTTGCGTATGTTA
C1-end	TTCTCATACGGACGCTTGTT
C2-start	GAGGAGGGTTGGTGTGTGTTA
C2-end	ATCCCCACCATCTCTTGTTC
C3-start	GTGTTGTAGTCATGCCGTC
C3-end	TGATAACCCCCATTCCCTGA
C4-start	CGGAAACACAAACACACAAC
C4-end	CCTCACCAACAAGCTGATAG
Gap C1-end/C2-end	Sequence 5'-3'
C1a-end	CTCTGGGATAAGCGTTGGAA
C2a-end	CACTTTCGTGTGTGTAGT

C1b-end	ATGACTCCACCAACACTAGC
C2b-end	CCGCAAGGCTAAAACCTCAA
C1c-end	CAAGTTGGTTCACGCCTTAG
C2c-end	GGTCTGGTTAGTACGCCTC
C1d-end	ACCTGTAATGTCAATGCCAC
C2d-end	CATCTCAGTACCCACAGGAA

Gap C2-start/C3-end Sequence 5'-3'

C2a-start	TCTCACCGACGTTCTAAACCC
C3a-end	TCCTTGACGGTACTTGCAG
C2b-start	CCGTATAACATCGTCTTGCAG
C3b-end	GACGTCAAATCATCATGCC
C2c-start	CTTGACCAGTGAGCTATTAC
C3c-end	GGAACATTGAACATAGATGC
C2d-start	CGCTACTTGGGATACCTCTC
C2e-start	GCCCCGAGCATCTATGTTCAA

Gap C1-start/C3-start Sequence 5'-3'

C1a-start	CTTGTGAGGTGAGGTAATGG
C3a-start	GTCTTAGCTTCCGGGTT
C1b-start	CAAGGCTAAAACCTAAAGGA
C3b-start	GATCCTCTCAAATTCCTGC
C1c-start	TGGGATCGGTGATTAGGAC
C3c-start	CTACACAAGCCACACCGAAC
C1d-start	GTCAATTCTCCGGCACTTC
C3d-start	TCATGCCTGCATTCTCACTC

21 **Supplementary figure legends**

22 **Figure S1.** Bidirectional best hit analysis performed in RAST [29].

23 **Figure S2.** Blast Dot Plot of *Agromyces aureus* AR33^T versus *Agromyces* sp. Leaf222 calculated in
24 RAST [29].

25 **Figure S3.** Heat map showing similarities between whole genomes of *A. aureus* AR33^T, other
26 *Agromyces* spp. and related members of the same family and phylum. The analysis was performed in
27 Gegenees [30]. The color profile goes from green (high similarity) to red (low similarity).

Figure S1

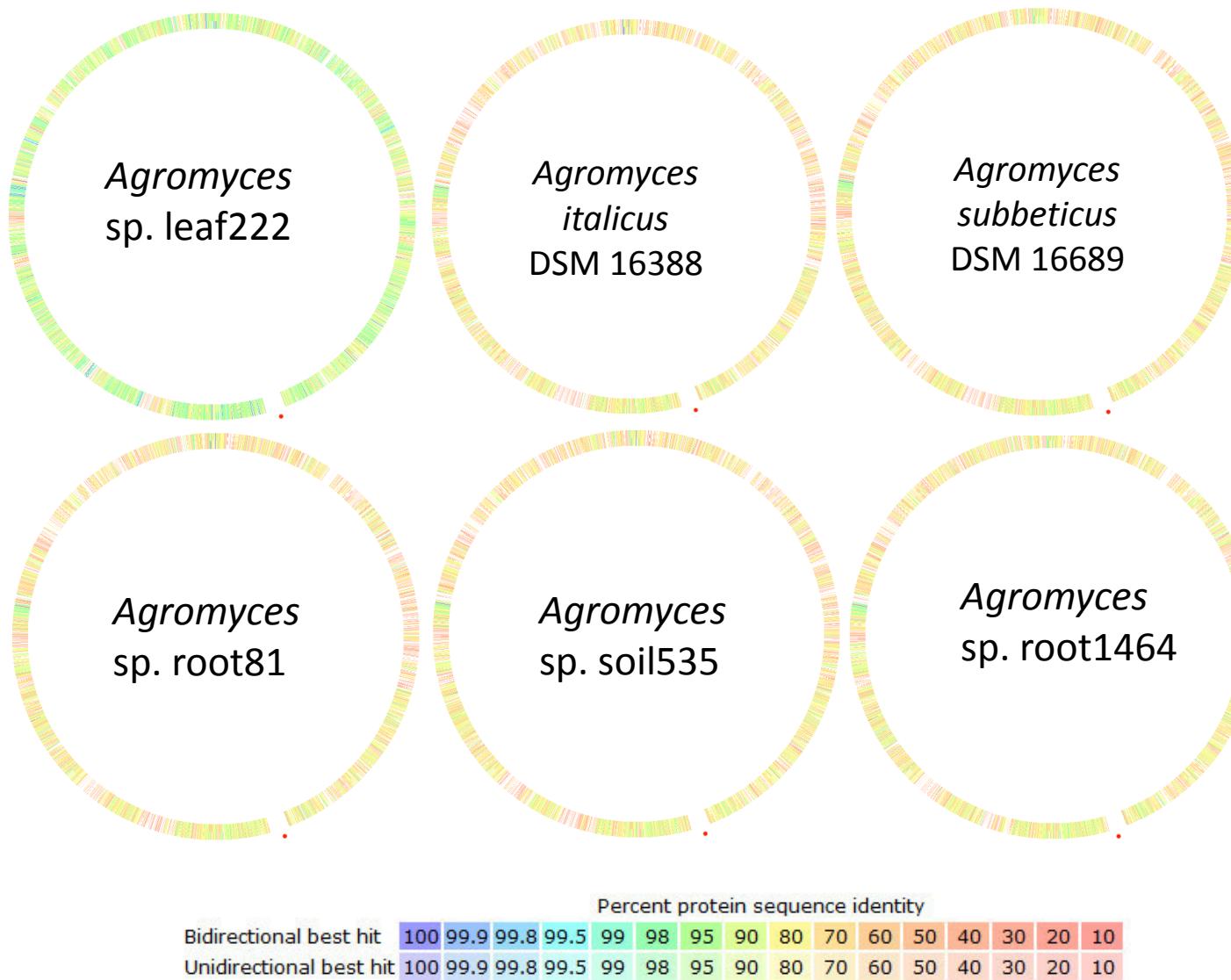


Figure S2

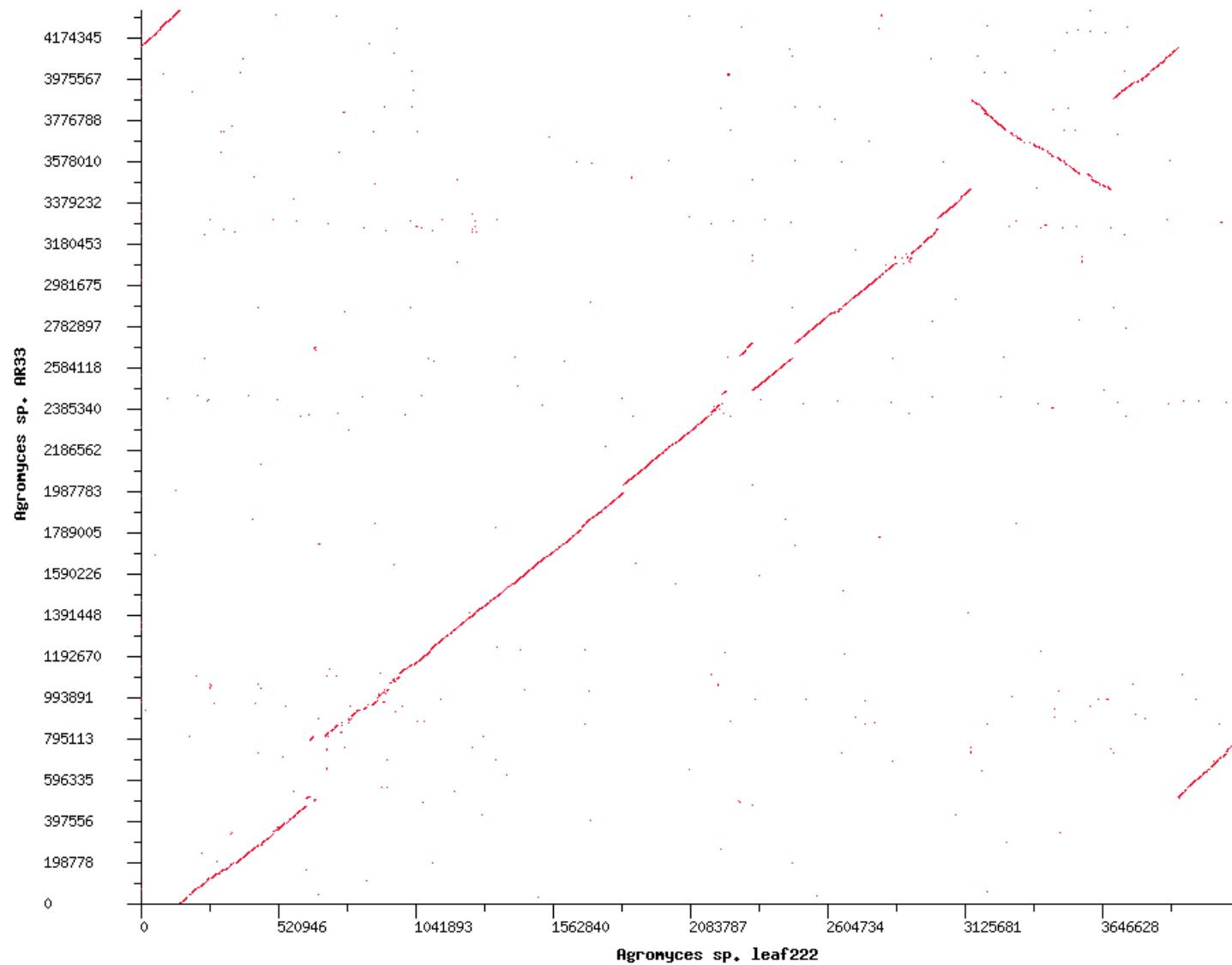


Figure S3

Organisms	1	2	3	4	5	6	7	8	9	10	11	12	13
1: <i>A. aureus</i> AR33	100	73	61	61	61	59	60	52	52	52	53	47	43
2: <i>Agromyces</i> sp. leaf222	73	100	60	62	62	60	60	51	51	51	53	46	42
3: <i>A. italicus</i> DMS 16388	60	60	100	62	62	60	60	52	51	51	52	45	42
4: <i>Agromyces</i> sp. root81	61	62	62	100	72	61	66	51	51	51	52	46	42
5: <i>Agromyces</i> sp. root1464	61	62	61	72	100	61	67	50	50	51	52	46	42
6: <i>Agromyces</i> sp. soil535	59	60	59	61	61	100	60	50	50	51	52	45	41
7: <i>A. subbeticus</i> DMS 16689	60	60	60	67	67	60	100	50	50	51	51	45	41
8: <i>Microbacterium testaceum</i> StLB037	52	52	52	52	51	51	51	100	55	50	52	46	43
9: <i>Microbacterium</i> sp. CGR1	51	52	51	51	51	51	50	55	100	50	52	47	44
10: <i>Clavibacter michiganensis</i> subsp. <i>michiganensis</i> NCPPB 382	52	52	52	52	52	51	52	50	50	100	53	46	43
11: <i>Leifsonia xyli</i> subsp. <i>xyli</i> CTCB07	52	53	52	52	52	52	52	50	50	51	100	46	43
12: <i>Cellulomonas flavigena</i> DSM 20109	46	47	47	47	47	46	46	47	47	46	47	100	46
13: <i>Streptomyces coelicolor</i> A3(2)	44	45	46	46	45	45	45	46	46	45	48	48	100